

FIGURE 1
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mTRT cDNA clone

- 3496 base pairs

-cDNA: nucleotides 10 to 3435

-ORF: nucleotides 39 to 3404

GAATTCCGGG	TGGGAGGGCC	ATCCCCGGCCT	TGAGGCACAAT	GACCCGGCGCT	50
CCTCGTTGCC	CCGGGGTGC	CTCTCTGCTG	CGCAGGCCAT	ACCGGGAGGT	100
GTGGCCGGCTG	GCAACCTTG	TGCGGGGCCCT	GGGGCCCCGAG	GGCAGGGGGC	150
TTGTGCAACC	CGGGGACCCG	AAGATCTACC	GCACCTTGGGT	TGCCCAATGC	200
CTAGTGTGCA	TGCACTGGG	CTCACAGCCT	CCACCTGCCG	ACCTTTCCCT	250
CCACCAGGTG	TCATCCCTGA	AAGAGCTGGT	GGCAGGGGT	GTGCAGAGAC	300
TCTGCCGAGCG	CAACGAGAGA	AACGGCTGG	CTTTGGCTT	TGAGCTGCTT	350
AACGAGGCCA	GAGGGGGGCC	TCCCATGGCC	TTCACTAGTA	GCCTGGCTGTAG	400
CTACTTGGCC	AACACTGTTA	TTGAGACCCCT	GCGTGTCACT	GGTGCATGGA	450
TGCTACTGTT	GAGCCGGAGTG	GGCGACGACC	CCTGCTGGCA	ACCAGGGTGTG	500
CACTGTGCTC	TTTATCTCT	GGTGGCCCCC	AGCTGTGCCCT	GGGAGGTG	550
TGGGTCTCCC	CTGTACCAAA	TTTGTGCCAC	CACGGATATC	TGGCCCTCTG	600
TGTCCGGCTAG	TTACAGGCC	ACCCGGACCCG	TGGGCAAGGAA	TTTCACTAAC	650
CTTAGGTTCT	TACAACAGAT	CAAGAGCAGT	AGTCGGCCAGG	AAGCACCGAA	700
ACCCCTGGCC	TTGCCATCTC	GAGGTACAAA	GAGGCATCTG	AGTCTCACCA	750
GTACAAGTGT	GCCTTCAGCT	AAGAAAGGCCA	GATGCTATCC	TGTCCCGAGA	800
GTGGAGGAGG	GACCCCCACAG	GCAGGGTGCTA	CCAACCCCAT	CAGGCAAATC	850
ATGGGTGCCA	AGTCCTGCTC	GGTCCCCCGA	GGTGCCTACT	GCAGAGAAAG	900
ATTGTCTTC	TAAAGGAAAG	GTGTCTGAC	TGAGTCTCTC	TGGGTGGGTG	950
TGCTGTAAAC	ACAAGCCCCAG	CTCCACATCT	CTGCTGTAC	CACCCGGCCA	1000
AAATGCCCTT	CAGCTCAGGC	CATTATTGA	GACCAGACAT	TCCCTTTACT	1050
CCAGGGGAGA	TGGCCAAAGAG	CGTCTAAACC	CCTCATTCT	ACTCAGCAAC	1100
CTCCAGGCCA	ACTTGACTGG	GGCCAGGAGA	CTGGTGGAGA	TCATCTTTCT	1150
GGGCTCAAGG	CCTAGGACAT	CAGGACCACT	CTGCAGGACA	CACCGTCTAT	1200

FIGURE 1
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mTRT cDNA clone
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CGCGTCCGATA	CTGGCAGATG	TCCAACAGCT	GCTGGTGAA	1250
CATGCAAGT	GCCAATATGT	AGGTCACATT	GCAGGGTTCG	1300
AAACAGCAAA	CAACAGGTGA	GAACACCAGC	CCACCGCACC	1350
TCATGGATT	GCTCCGCTG	CCTGGCAGGT	ATATGGTTT	1400
CTCTGGCCT	GTCTCTGCAA	GCTAGTCTCT	GGGGTACCAAG	1450
GCACAAATGAG	CGCCCGCTCT	TTAAGAACTT	ATCTCGTTGG	1500
GGAAATACGG	CAAGCTATCA	CTGCAGGAAC	GATGAAAAGTA	1550
GAGGATTGCC	ACTGGCTCCG	CAGCAGCCCC	GTGTCCCCGC	1600
TGCAGAGCAC	CGTCTGAGGG	AGAGGATCCT	CTGTTCTGGC	1650
TGATGGACAC	ATACGTGGTA	CAGCTGCCTA	TTACATCACAA	1700
GAGAGCACAT	TCCAGAAGAA	TTCTACCGTA	AGAGTGTGTG	1750
GAGCAAGCTG	CAGAGCATTG	ACACCTTGAG	AGAGTGGGGC	1800
TACGGGAGCT	GTCAACAAGAG	ATCACCCAGGA	CACCTGGCTA	1850
GCCATGCCCA	TCTGCAGACT	CCCCAAGGCCA	ACGGCCTGGG	1900
GCCCCATTGTG	AAACATGAGTT	TACCAAGACT	TTGGGCAGAA	1950
GGAAAGCAGGC	CCAGCATTTC	TCAAAGACTCT	CTTCAGCATTG	2000
CTCAACTATG	AGGGGACAAA	CTTATGGGGT	CTTCGTGTACT	2050
GGGTATGAAT	GACATCTACA	GGCCTTGTG	CTGCCTGTGCG	2100
GTGCTCTGGA	CCAGACACCC	TTGTTAAGGC	AGATGTGACC	2150
GGGGCCTATG	ATGCCATCCC	CTGGTGGAGG	TTGTTGCCAA	2200
TATGATCAGG	CACTCGGAGA	TATCCGCCAG	TATGCAGTGG	2250
TCCGGAGAGA	TAGCCAAGGC	AGTCCTTAG	GAGACAGGTC	2300
ACCAACCTCT	CTGACCTCCA	GGCCAGTTCC	TTAAGCATTCT	2350
GCAGGATTC	GATGCCAGTG	CTCCGTTGTC	ATCGAGCAGA	2400

FIGURE 1
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m^{RT} cDNA clone

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GCATCTCTAT	GAATGAGAGC	AGCAGGCAGCC	TGTTTGACTT	CTTCTGCAC	2450
TTCTTGGTCTC	ACAGTGTCTG	AAAGATTGGT	GACAGGTGCT	ATACGCAGTG	2500
CCAGGGCATC	CCCAGGGGCT	CCAGGCTATC	CACCCCTGCTC	TGCAGTCTGT	2550
GTTTCGGAGA	CATGGAGAAC	AAGCTGTTTG	CTGAGGTGCA	GCGGGATGGG	2600
TTGCTTTTAC	GTTTTGTTGA	TGACTTTCTG	TTGGTGACGC	CTCACCTTGGG	2650
CCAAGCAAAA	ACCTTCCCTCA	GCACCCCTGGT	CCATGGGGTT	CCTGAGTATG	2700
GGTGCATGAT	AAACTTGCAG	AAGACAGTGG	TGAACCTCCC	TGTGGAGCCT	2750
GGTACCCCTGG	GTGGTGCAGC	TCCATAACCAG	CTGCCCTGCTC	ACTGCCTGTT	2800
TCCCTGGGTGT	GGCCTGCTGC	TGGACACTCA	GACTTTGGAG	GTGTTCTGTG	2850
ACTACTCAGG	TTATGCCAG	ACCTCAATTAA	AGACGAGCCT	CACCTTCCAG	2900
AGTGTCTTCA	AAGCTGGAA	GACCATGCGG	AACAAAGCTCC	TGTGGGTCTT	2950
GCGGTTGAAG	TGTCACTGGTC	TATTTCCTAGA	CTTGAGGTG	AACAGCCTCC	3000
AGACAGTCTG	CATCAATATA	TACAAGATCT	TCCTGCTCA	GGCCCTACAGG	3050
TTCCATGCAT	GTGTGATTCA	GCTTCCCTTT	GACCAAGCGTG	TTAGGAAGAA	3100
CCTCACATT	TTTCTGGGCA	TCATCTCCAG	CCAAGCATCC	TGCTGCTATG	3150
CTATCCTGAA	GGTCAAGAAAT	CCAGGAATGA	CACTAAAGGC	CTCTGGCTCC	3200
TTTCCTCCCTG	AAGCCGGACA	TTGGCTCTGC	TACCAAGGC	TCCTGGCTCAA	3250
GCTGGCTGCT	CATCTGTCA	TCTACAAATG	TCTCTGGGA	CCTCTGAGGA	3300
CAGCCCCAAA	ACTGCTGTGC	CGGAAGCTCC	CAGAGGGCAC	AATGACCATC	3350
CTTAAAAGCTG	CAGCTGACCC	AGCCCTAACG	ACAGGACTTTC	AGACCAATT	3400
GGACTAACCC	TGTCTCCTTC	CGCTAGATGA	CGCTAGAGGG	CGAATTCCAG	3450
CACACTGGCG	GCCGTACTA	GTGGATCCGA	GCTCGGTACCC	AAGCTT	3496

015389-003110US

FIGURE 2

1122 Amino Acids
127,979 kD
pI ~ 10.4

MTRAPRCPAV RSLLRSRYRE VWPLATFVRR LGPEGRRLVQ PGDPKIRYRTL VAQCLVCMHW GSOPPPADLS FHQVSSLKEL 80
VARVVQRLCE RNERNVLAFG FELLNEARGG PPMMAFTSSVR SYLPNTVIET LRVSGAWMILL LSRVGDDLLV YLLAHCALYL 160
LVPPSCAYQV CGSPLYQICA TTDIWPSVSA SYRPTRPVGR NFTNLRFLQQ IKSSSRQEAP KPLALPSRG T KRHLSLTSTS 240
VPSAKKARCY PVPVVEEGPH RQVLPTPSGK SWVPSPARSP EVPTAEKDLS SKGKVSDLIS SGSVCKHKP SSTSLLSPPR 320
QNAFQLRPF1 ETRHFLYSRG DGQERLNPSF LLSNLQPNLT GARRLVEIIF LGSRRPRTSGP LCRTHRLLSRR YWQMRPLFQQ 400
LLVNHAECQY VRLLRSHCRF RTANQQVTD A LNTSPPHLM D LRLHSSPWQ VYGFRLRACLC KVVSASLWGT RHNERRFFKN 480
LKKFISLGKY GKLSLQELMW KMKVEDCHWV RSSPGKDRVP AAEHRLRERJ LATFLFWLMD TYVVQLLRSF FYITESTFQK 560
NRLFFYRKSV WSKLQSIGVR QHLERVRLRE LSQEDEVRHHQ DTWLAMPICR LRFIPKPNGL RPIVNMSYSM GTRALGRRKQ 640
AQHFTQRLKT LFSMLNYERT KHPHLMGSSV LGMNDIYRTW RAFVLRVRA DQTPRMYFVK ADVTGAYDAJ PQGKLVEVVA 720
NMIRHSESTY CIRQYAVVRR DSQGQVHKSF RRQVTTLSDL QPYMGQFLKH LQDSDASALR NSVVIQESIS MNESSSSLFD 800
FFLHFLRHSV VKIGDRCYTQ CQGIPQGSSL STLLCSLCFG DMENKLFAEV QRDGLLRFV DDFLLVTPHL DQAKTFLSTL 880
VHGVPPEYGCINLQKTVVNF PVEPGTLLGGA APYQLPAHCL FPWCGLLLDT QTLEVFCDYS GYAQTSIKTS LTFQSVFKAG 960
KTMRNKLSSV LRLKCHGLFL DLQVNLSIQT V CINIYKIFLL QAYRFHACVI QLPFDQRVRK NLTFFLGHS SQASCCYAIL 1040
KVKNPGMTLK ASGSFPPEA HWLCYQAFLL KLAAHSVIYK CLLGPIRTAQ KLLCRKLPEA TMILKAAAD PALSTDFQTI 1120
LD 1122

FIGURE 3

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mTRT vs. hTRT amino acid alignment

mTRT MTRAPRCPAVRSILLRSRYREWWPLATFVRRRLGPEGRRRLVQPGDPKIVRTLVHQVCLVCMHWGSQPPPQPADLSFHQVS
hTRT MPRAPRRCRAVRSSLRSHYREVILPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPWDARPPAAPSFRQVS

SLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVRSYLPNTVIETLKVSGAWMLL SRVGDDLLV
CLKELVARVLQRLCERGAKNVLAFGFAALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLV

YLLAHCALYLLVPPSCAYQVCGSPLYQICATTDIWPSVSASYRPTRPVGRNFTNLQKSSRQEAPKPLAL
HLLARCALFVLVAPSCAYQVCGPPLYQLGAATQARPPHAS.GPRRRLG CERAWNHSVREAGVPLGL

PSRGTKRHLSLTSTSVPSSAKKARCYPPRVEEGPHRQVLPTPSGKSWVSPARSPEVP..TAEKDLSSKGKVSD
PAPGARRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSPDRGFCVVSPARPAEEATSLEGALSG

LSLSGSVCCCKHKPSSSTSLLSPRQNAFQLRP.FIETRHFLYSRGDGQERLNPSFLLSNLQPN LTGARRLVEIF
TRHSHPSVGRQHHAGCPPSTSRRPRPWDTCPVVAETKHFLYSSGD.KEQLRPSFLLSLRPSLTGARRLVEITIF

LGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQYVRLRSHCRFRTA..... NQQVTDAA
LGSRPWNMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPKQGSVAAPEE

FIGURE 3
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mTRT vs. hTRT amino acid alignment

LNTPSPHLM DLLRHSSPWQVYGFRLRACLCKVVSASLWGTRHNERRFKNLKKFISLGKYGKLSLQELMWKMKVEDTDPRLVQLLRQHSSPWQVYGFVRACLRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSSLQELTWKMSVR

Motif T

DCHWLRRSSPGKDRVPAAEHLRERILATFLFWLMDTRYVQLRSFFYITESTFQKNRLFFYRKSVWSKQLQSIGVR
DCAWLRRSSPGVGCVPAAEHLREELAKFLHWLMSVYVSELLRSFFYVTETTFQKNRLFFYRKSVWSKQLOSIGR

Motif 1

QHLERVRLLRELSQEVRHHQDTWLAMPICRLRFIPKPNGLRPIVNMSYSMGRKQAOQHFTORLKTLSMIL
QHIIKRVQLRELSAEVRQHREARPALLTSRRLRFIPKPDGLRPIVNMDYVVGARTFREKRAERLTSRVKALFSV

Motif A

NYERTKHPHLMGSSVLMGNDIYRTWRAFVLRVRAFDQTTPRMYFVKADVTGAYDAIPQGKLVEVVANMIRHSESTY
NYERARRPGLLGASVGLGLDDIHRRAWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVLAIIK.PONTY

CIRQYAVVRRDSQQVHKSFRRQVTTLSDLQPYMGQFLKHLQDSDASALRNSVVIQSQISMNESSSSLFDFFLHF
CVRRYAVVQKAAGHVRKAFKSHVSTLTDLQPYM/RQFVAHLQET..SPLRDAVVIQEOSSLNEASSGLFDVFLRF

Motif B

Motif C Motif D

RHSVVKIGDRCYTCQGPQGSSLSTLLCSLCFGDMENKLF
MCHHAVRIRGKSYVQCQGPQGSILSTLLCSLCYGD
MENKLFAGIRRDGLLRLVDDFLLVTPHLTHAKTFLRTL
LRFVDDFLLVTPHLTHAKTFLRTL
LRAVLL

FIGURE 3
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mTfRT vs. hTfRT amino acid alignment

Motif D	Motif E
VHGVPEYGC <u>MINL</u> Q <u>KTV</u> NFPVEP <u>GT</u> LGGAAP <u>YQL</u> PAH <u>CL</u> FP <u>WC</u> GL <u>LL</u> DT <u>Q</u> T <u>LE</u> V <u>FC</u> CD <u>YSG</u> YA <u>QTS</u> IK <u>T</u> SL <u>TF</u> Q <u>S</u>	
VRGVPEYGC <u>VVN</u> LR <u>KTV</u> NFPVE <u>D</u> ALGGTAFVQ <u>Q</u> MP <u>AH</u> GL <u>FP</u> WC <u>GL</u> <u>LL</u> DT <u>R</u> T <u>LE</u> V <u>Q</u> SD <u>YSS</u> ART <u>SIR</u> A <u>SL</u> TF <u>NR</u>	
VFKAGK <u>TM</u> RN <u>KL</u> LS <u>VL</u> RL <u>KC</u> H <u>GL</u> <u>FL</u> DL <u>QV</u> NS <u>L</u> Q <u>T</u> VC <u>C</u> IN <u>IY</u> K <u>F</u> LL <u>Q</u> AY <u>YR</u> F <u>H</u> AC <u>V</u> I <u>Q</u> LP <u>F</u> D <u>Q</u> R <u>V</u> R <u>K</u> N <u>L</u> T <u>FF</u> L <u>GI</u> S	
GF <u>KAGR</u> N <u>MR</u> R <u>KL</u> FG <u>VL</u> RL <u>KC</u> HS <u>SL</u> FL <u>DL</u> Q <u>VN</u> SL <u>Q</u> TV <u>C</u> T <u>N</u> IY <u>K</u> ILL <u>Q</u> AY <u>YR</u> F <u>H</u> AC <u>V</u> I <u>Q</u> LP <u>F</u> H <u>Q</u> V <u>W</u> K <u>N</u> P <u>T</u> FF <u>L</u> R <u>V</u> IS	
SQASCCY <u>A</u> IL <u>K</u> V <u>K</u> N <u>P</u> GM <u>T</u> L <u>K</u> AS <u>G</u> S...FP <u>PE</u> AA <u>H</u> W <u>L</u> C <u>Y</u> Q <u>A</u> F <u>FL</u> L <u>K</u> LA <u>A</u> H <u>S</u> V <u>I</u> Y <u>K</u> CL <u>I</u> G <u>P</u> LR <u>T</u> A <u>Q</u> K <u>L</u> C <u>R</u> K <u>L</u> P <u>E</u> AT <u>M</u>	
DT <u>ASL</u> C <u>YS</u> IL <u>K</u> AK <u>N</u> A <u>G</u> M <u>S</u> L <u>G</u> A <u>K</u> G <u>A</u> G <u>PL</u> P <u>SE</u> A <u>V</u> Q <u>W</u> L <u>CH</u> Q <u>A</u> F <u>FL</u> L <u>K</u> TR <u>H</u> R <u>V</u> T <u>Y</u> V <u>P</u> L <u>LG</u> S <u>R</u> T <u>A</u> Q <u>T</u> Q <u>L</u> S <u>R</u> K <u>L</u> P <u>G</u> T <u>TL</u>	
TL <u>K</u> AA <u>A</u> D <u>P</u> A <u>L</u> S <u>T</u> D <u>F</u> Q <u>T</u> ILD 1122	
TA <u>L</u> E <u>A</u> A <u>N</u> P <u>A</u> L <u>P</u> S <u>D</u> F <u>K</u> TILD 1132	

FIGURE 4
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	TRT con	WL	V	LL	FFY	TE	R	YYRK	W	L	I	Motif T
hTRT/hEST2p		WLMSVYVVELLRSFFYVTE	TFQKNRLLFFYRKSVW	SKLQSIGIRQHLK								
mTRT		WLMDTYVVQLLRSFFY	TESTFQKNRLLFFYRKSVW	SKLQSIGIRQHLK								
Ea_p123		WIFEDLVVSLIRCFYV	TEQQKSYSKTYYYRKNIW	DVIMKMSIADLK								
Sc_EST2p		WLFRQLIPKIIQTF	FFYCTEISSTVT-	IVYFRHDTWINKLITP	FIVEYFK							
Sp_Trlp		WLYNFSFPIIQLQSF	FFYITESSDLRNRTVY	FRKDIWKLLCRP	FITSMKM							
	TRT con	LR	IPK	RI			R	I			K	Motif 2
hTRT/hEST2p		EVRQHREARPALLTSR	LRFIPKPDG		LRPIVNMMDYVVGART	FREKRAERL	TSRV					
mTRT		EVRHHQDTWLAMPICR	LRFIPKPNG		LRPIVNMMSYSM	GTRALGRRKQAOQHFT	ORL					
Ea_p123		KEVEEWKKSLGFAPGK	LRLIPKKTT		FRPIMTFNKKIVNSDRK	TTKLT	TTNTKLL					
Sc_EST2p		CRNHNSYTLNSNFNHSK	MRIPKKSNN		FRIAIPCRGAD	EEFTIYKENHKNAI	QP					
Sp_Trlp		NNVRMDTQKTTLPPA	VIRLLPKNT		FRLITNLRKREI	IKMGSNK	KMLV	VSTNQ				
	TRT con	P	YF	K	DV	YD	I					Motif A
hTRT/hEST2p		PPPELYFV	KV	DVTGAY	DTIPQDRL	TEVIASI	I	KP				
mTRT		QTPRMYFV	KADVTGAY	DAIPQGKL	VEVVANMIRH							
Ea_p123		GQPKLFFATM	DIEKCYDSV	NREKLSTFLKTT	KL							
Sc_EST2p		VLPELYFMKF	DVKSCYDSI	PRMECMRLKDALKN								
Sp_Trlp		FGRKKYF	VRIDKSCYDRIK	QDLMFRIVKK	KLKD							

FIGURE 4
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	Motif B'	Motif C	Motif D	Motif E
TRT con	K Y Q GIPQ GS LS L Y D	LLR DDFLL IT		
htt/hEST2p	KSYVQCQGIPQGSILSTLLCSILCYGDMENKLFAGI	LLRLVDDDFLLVTPHLTH		
mTRT	RCYTQCQGIPQGSILSTLLCSILCFGDMENKLFAEV	LLRFVDDDFLLVTPHLDDQ		
Ea_p123	KFYKQTKGIPQGLCVSSILSSFFYYATLEESSLGFL	LMRLTDDYLLITQENN		
Sc_EST2p	KCYIREDGLFQGSILSAPIVDLVYDDLLEFYSEFK	ILKLAADDFLJISTDQQQQ		
Sp_Trlp	SQYLQKVQGIPQGSILSSFLCHFYMEDLIDEYLSTT	LLRVVDDDFLFITVNKKD		
TRT con	A F G	N K		
htt/hEST2p	AKTFLRTLVRGVPEYGCVVNLRKTVV	HGLFPWCGLLL		
mTRT	AKTFLSTLVHGVPEYGCMINLQKTVV	HCLFPWCGLLL		
Ea_p123	AVLFIEKLINVSRENGFKFNMKKLQT	QDYCDWIGISI		
Sc_EST2p	VINIKKALAMGGFQKYNAKANRDKILA	KELEVWKHSST		
Sp_Trlp	AKKELNLSLRGEKHNFSSTSLEKTVI	KKRMPFFGFSV		

FIGURE 5
General and Murine Specific TERT Amino Acid Motifs

x_n - any aa

h = A, L, I, V, P, F, W, M

p = G, S, T, Y, C, M, Q

c = D, E, H, K, R.

r ₁ , = I, L	r ₅ = F > L	r ₉ = R > K	r ₁₃ = G > H	r ₁₇ = T > S
r ₂ = R, Q	r ₆ = P > F	r ₁₀ = G > V	r ₁₄ = C > A	
r ₃ = Y > F	r ₇ = S > L	r ₁₁ = N > S	r ₁₅ = I > V	
r ₄ = K > H	r ₈ = L > M	r ₁₂ = W > F	r ₁₆ = L > V	

">" = 1st aa preferred over the 2nd

gen = general TERT motif

hum = human specific motif

mus = mouse specific motif

bold residues are species specific changes

Motif T

gen	W-r ₁ -x ₄ -h-h-x-h-h-r ₂ -p-F-F-Y-x-T-E-x-p-x ₃ -p-x _{2,3} -r ₃ -r ₃ -R-r ₄ -x ₂ -W
hum	W-r ₁ -x ₄ -h-h-x-h-h-r ₂ -p-F-F-Y-V-T-E-x-p-x ₃ -p-x _{2,3} -r ₃ -r ₃ -R-r ₄ -x ₂ -W
mus	W-r ₁ -x ₄ -h-h-x-h-h-r ₂ -p-F-F-Y-I-T-E-x-p-x ₃ -p-x _{2,3} -r ₃ -r ₃ -R-r ₄ -x ₂ -W

Motif 1

gen	h-R-h-r ₁ -P-K-x ₂ -p
hum	h-R-h-r ₁ -P-K-x-D-p
mus	h-R-h-r ₁ -P-K-x-N-p

Motif 2

gen	r ₅ -R-h-I-x ₂ -h
hum	"
mus	"

Motif A

gen	P-c-x-r ₃ -F-h-x-h-D-h-x ₂ -r ₁₄ -Y-D-x-r ₁₅
hum	P-E-x-r ₃ -F-h-x-V-D-h-x ₂ -r ₁₄ -Y-D-x-r ₁₅
mus	P-R-x-r ₃ -F-h-x-D-D-h-x ₂ -r ₁₄ -Y-D-x-r ₁₅

Motif B'

gen	Y-x-r ₂ -x ₂ -G-r ₁ -r ₆ -Q-G-r ₇ -x-r ₁₆ -S-x-h-r ₁
hum	Y-x-r ₂ -x ₂ -G-r ₁ -r ₆ -Q-G-r ₇ -I-r ₁₆ -S-x-h-r ₁
mus	Y-x-r ₂ -x ₂ -G-r ₁ -r ₆ -Q-G-r ₇ -S-r ₁₆ -S-x-h-r ₁

Motif C

gen	r ₁ -r ₈ -r ₉ -h-x-D-D-r ₃ -L-h-R ₁₅ -R ₁₇
hum	r ₁ -r ₈ -r ₉ -L-x-D-D-r ₃ -L-h-R ₁₅ -R ₁₇
mus	r ₁ -r ₈ -r ₉ -F-x-D-D-r ₃ -L-h-R ₁₅ -R ₁₇

Motif D

gen	r ₁₀ -x ₂ -c-x-p-x ₃ -r ₁₁ -x ₂ -K-x ₃
hum	r ₁₀ -x ₂ -c-x-p-x ₃ -r ₁₁ -R-K-x ₃
mus	r ₁₀ -x ₂ -c-x-p-x ₃ -r ₁₁ -Q-K-x ₃

Motif E

gen	r ₁₂ -x-r ₁₃ -x-r ₇ -x
hum	"
hum	"

mTRT Promoter Region
-cDNA start at 1680
-ORF start at 1709

FIGURE 6
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AAAGCAGGCC	TGTAACACAA	AGGTCCCTTT	TCCTGGTTA	TCGGGTGTTA
TAGACAAATT	CCACTTGGTT	TCCACTTCAG	TTTTTCTAC	TGCACCCCTT
TTGGATTCTG	ATGCTTGAAC	CCAGGTTGGT	AGTCAGCAAG	CCCAAGTGGGA
CCTTCTTT	CTTGGTTTT	TTGAGGCAGG	TCTCATTTTG	TCATCCTGCT
CCTAAATTTC	AGCATGTAGT	GGCTGGTTTN	GAATGCTTT	CCGGCGATAT
NTACTTCCCA	AGAGTAGCTA	ACAAGTGTGC	ACCACCATGC	GAACTACACT
TTTTATTTTT	GAGACTGTTT	TCTATGCTGG	TTTCTTTGGG	TCTTATTTT
AAGGTAGCTT	ACAAGTGTGC	ACCACCATGC	CCCGCGATAT	AAGGTAGCTT
GAGACTGTTT	TCTATGCTGG	TTTCTTTGGG	GAACTACACT	TAAGTAGCAG
ATAAATTCT	ATAAATTCT	CAGTCAGGC	CCATATCTCT	GATGTCCTACT
AATCTTCAA	AATCTTCAA	CAAACCCCTT	CAAAAGAACT	TACCAAGGGCG
CTAAAATAGC	CTAAAATAGC	TCCCTGTAAT	CCTGAGCATT	TTCAAATGCT
TATAAGGGAG	TATAAGGGAG	TAATATGAA	AACGGCCCTG	CACCAAAGGT
ATAGAAGCAA	ATAGAAGCAA	TTTCCTCAGA	AAGCTGAAGG	AGTAGAGATC
AGCATTTCAG	AGCATTTCAG	TGTTGCCAA	ACTCAGGCTAC	CCTCTCTAAC
TATTTCCCAG	TATTTCCCAG	AGATCAAA	TTCAGCAGCC	ACCCCCACCC
AGTCGGTGG	AGTCGGTCA	TTACATATGC	CCCAACAAACA	TTGCCAACCT
TATATTGTT	ACGTGCAAGT	ACGTGCAAGT	ACTATCACAG	
ACAGATTCCC	CCATCCTAAC	GTCCGAGGTCG	CCGCTTTGGC	
TATGGCTCAG	CTCACCCAAAT	GGCCCTGGCC	TTGCTATGGG	
CTATCCTACC	TCTGGACTCT	GAGGTGAAGG	CCACTGGAAC	
AGCAGAGCTG	CCATCCTAAC	TAGGTCCCCCT	TCCTTGGTG	
GGCAAGGCC	CTCACCCAAAT	GGAGGTGTATG	GTCCGCACAC	
GAGATGATGC	TCTGGACTCT	GGAGGTGTATG		
GCTAACCGAG	GGCTTTTAC			
ACGAAACATA	TTTGGGATCT			

50
100
150
200
250
300
350
400
450
500
550
600
650
700
750
800
850
900
950
1000
1050
1100
1150

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FIGURE 6
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TAACCTAT	AGTAGAATGT	TCAGCTGTAA	TCATTAAGAA
CACCACCCAC	CTCACTGTCT	GTGTCAACCA	CAGCAGGCTG
CTCAGGAACA	GGCAAACACT	TAGGTCCCTCC	GCCTACCTAA
ATCAAGGATA	GGCTTCTTTG	CTTGCCCCAA	CCTCGCCCCA
CCTGGGGATT	CCCAGCTCAG	GGGAAAAGG	AAGCCCCGAGA
AGAGGGAAAT	CCTGCATGAG	TGCGCCCCCT	TTCGTTACTC
AGCAACCACT	GAACTTGGCC	GGGGAACACA	CCTGGTCCCTC
ATTGTGACCA	TCAAACGGAAA	AGTACTATTG	CTGGGACCCC
CTACAACGCT	TGGTCCGGCCT	GAATCCCCGC	CCTTCCTCGG
CATCTTTTC	GTCGTGGACT	CTCAGTGGCC	TGGGTCTGG
AGCACACCCCT	TGCATCTTGG	TTCCCGCACG	TGGGAGGGCCC
TGAGGCACAAAT	GACCCGGGCT	CCTCGTTGCC	CCGGGGTGGC
CGCAGCCGAT	ACCGGGAGGT	GTGGGCCGCTG	GCAACCTTGTG
GGGGCCCG			1808

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FIGURE 7
mTERT Genomic DNA

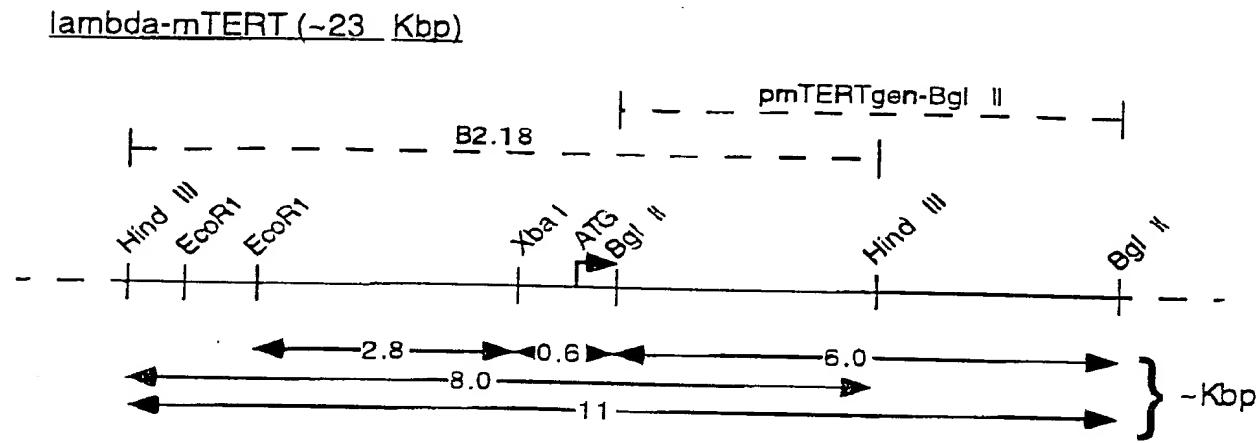


FIGURE 8
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Preliminary sequence of B2.18, containing the promoter region of mTERT.
cDNA starts at: 2057
ORF starts at: 2087

AAACAAAGTC AATGAGGAAT GGCTGTGTT CATCTGACC ACTGAGAAGT
AAAACCGGGT GCAGTGTGTT CCAAAAGGC AAGGTGACAG CAGAGGGAG 50
GCCCCAATCT AGAGCAGGGC CTTCGGTGTTG AATGGGGAG ATCAAACGGG
AGTTGGTTTC TGCCAGCAG CGAGAGTCCA TAGGGGTAGC GACACCGAG 100 150
CCGAGGATTG TTACACTCTT CCCTGAGGG GAGATGACTT TTACACAGT CGTTTATGG
TCACACTCTT AAAGTTCTTA GGGGAGCCC CTCCCCAAA AGGCTCTCCC 200 250
AGGCTCTTAAAGCA CAGCTTTTA AAGCAGGCC GTAAAGCACA AAGGATCCCG 300 350
ATCCTGGCT TCATGTTGG CTGGTAGACA ACTTCACACT GTTTTCCACT 400 450
TCAGTTCTT CTAACCTCTT TGTTATTGTA TTCTGTATGCT TGAACCCAGG
GTGTTGTTAGT CAGGAAGTGC TACCCCCCTC TCCTCTCTT TGTTTTTTG 500 550
AGGCAGGGTC TCATTTGTC CAAGTGGAC TAAATTTCAG CATGTAGCTG
GCCTGGTTT GAATGCCCTC TCATCCCTGC TCTACTTCCC AAGAGTAGCT 600 650
TACAAGTGTG CACCACCATG CCCCGCGATA TTCTTATTT TGAGACTGTT 700
TCTATGCTG GTTCTTTGG GGAACATCAC TAAGGTAGCT TACAAGTGTG 750
CACCACATG CCCCGCGATA TTCTTATTG TGAGACTGTT TCTATGCTG 800 850
GTTTCTTGG GGAACATCAC TAAGGTAGCT TCATTTGTTG CATAAATTTC
TCAGTTCAAG CCCATATCTC CTAAGTAGCA GAACTAAGCA AATCTAAAC 900
AACCCCTCA AAAAGACTGA TGTCACACTA ACGGACTCTT AAAATAGCTC 950
CCTGTAATTC TGAGCATTAA CAAGGGGCA GACCTCTTAAAGGGAGTA
ATATGAAAC GGCCTGTT AAATGCTAGG TCGGTTGATA GAAGCAATT 1000
CCTCAGAAAG CTGAAGGCC CAAAGGTTAT ATTGTGTTAGC ATTTCAGTGT 1050
TTGCCAAACT CAGCTACAGT AGAGATCACA GATTCCCTAT TTCCAGAGA 1100
TTCAAATTTC AGCAGCCCT CTCTAACTAT GGCTCAGAGT CGGTCTATTA 1150 1200
CATATGCCCA AACAAACACC CCACCCCTA TCCTACCCCC GCCTCACACG
TGCAAGTACT ATCACAGTTG CCAACCTAGC AGAGCTGCCA TCTAAAGGTC 1250 1300
GAGGTGCGCG CTTGGCTGT GTGCACAGGG AAGGGCCCTC ACCCAATGGC 1350
CCTGGCCTTG CTATGGTGC GTGAGTTGAG ATGATGCTCT GGACTCTGAG 1400

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FIGURE 8
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GTGAAGGCCA	CTGGAACAGT	GAAAAAAGCT	AACGCAGGGC	TTTTACCTAG	1450
GTCCCCCTTCC	TTGGGGGGTG	GGTGTGTTAGG	GAACATATTG	GGGATCTGGA	1500
GTGTATGGTC	GCACCAAAAT	AAAGCCTAA	CCTATATAGT	AGAATTTCAG	1550
CTGTAATCAT	TAAGACTGA	GATTGCCACC	ACCCACCTCA	CTGTCGTGTT	1600
CAACCACAGC	AGGCTGGAGC	AGTCAGCTCA	GGAACAGGCA	AAACCTTAGG	1650
TCCCCTCGCC	TACCTAACCT	TCAATACATC	AAGGATAGGC	TTCTTTGCTT	1700
GCCCCAAACCT	CGCCCCAGTC	TAGACCACCT	GGGGATTCCC	AGCTCAGGGC	1750
GAAAAGGAAG	CCCGAGAACG	ATTCTGTAGA	GGGAATACTCT	GCATGAGTGC	1800
GCCCCCTTTC	GTTACTCCAA	CACATCCAGC	AACCCTGAA	CTTGGCCGGG	1850
GAACACACCT	GGTCCTCATG	CACCAAGCTT	GTGACCATCA	ACGGAAAAGT	1900
ACTATTGCTG	CGACCCCGCC	CCTTCCGCTA	CAACGCTTGG	TCCGCCCTGAA	1950
TCCCGCCCT	TCCTTCGTTTC	CCAGCCTCAT	CTTTTCGTC	GTGGACTCTC	2000
AGTGGCCTGG	GTCCTGGCTG	TTTCTTAAGC	ACACCTTGC	ATCTTGGTTC	2050
CGGCACGTG	GAAGGGCCAT	CCGGGCCTTG	AGCAAAATGA	CCCGGGCTCC	2100
TCGTTGCC	GCGGTGGCT	CTCTGCTGGC	CAGCCGATAC	CGGGGGTT	2150
GCCCCGTTGGC	AACCTTTGTG	CGGGCCTGG	GGCCCCGGGG	CAGGGGGCTT	2200
GTGCAACCCG	GGGACCGAAG	ATCTACCGCA	CTTTGGTTTG	CCCAATGGCT	2250
ACTGTGCATG	CACTGGGCT	CAACGGCTTC	ACCTGGCGAC	CTTTCCTTCC	2300
ACCAAGGTGGG	CCTCCAGGGC	GGATCCCCAT	GGGTCAAGGG	CGGAAAGGCC	2350
GGAGGGACGTG	GGATAGTGTG	TCTAGCTCAT	GTGTCAAGAC	CCTCTTCTCC	2400
TTACCAAGGTG	TCATCCCTGA	AAAGAGCTGG	TGGCCAGGGT	TGTGCAGAGA	2450
CTCTGGGAGC	GCAACGAGAG	AAACGTGCTG	GCTTTGGCT	TTGAGGTGCT	2500
TAACGAAGGC	AGAAGGGGC	CTCCCATGGC	CTTCACATAAT	TAGGGTGGCT	2550
AAGCTACTTG	CCCAACACTG	TTATTGAAA	CCTGGGTGTC	AGTGGTGCAT	2600
GCATGCTACT	GTTGAGCCGA	ATGGGGGACA	CCTGGGTGGC	TACCTGCTGG	2650
C					2651

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FIGURE 9
mTERT Genomic DNA

pmTERTKO

